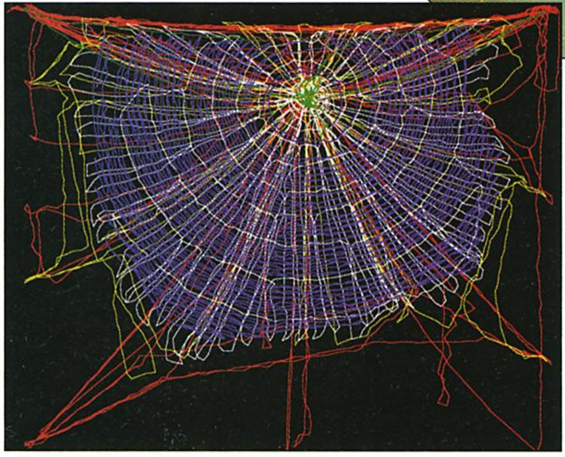
MOLECULAR GENETICS

Spider Genes Reveal Flexible Design

As engineers, spiders leave most other creatures in the dust. Dragline silk, which the eight-legged acrobats use for bungee jumping or rigging webs, is fabulously strong; a cable not much thicker than a garden hose could support two fully loaded Boeing 737 jetliners without breaking. And yet the so-called flagelliform silk used in web spirals is elastic enough to stretch over 200%. With seven kinds of silk, many spiders weave complex and resilient works of art.

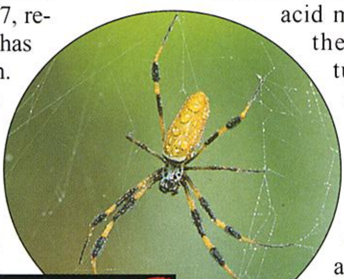
Now, the most extensive look yet at spider-silk DNA, reported on page 1477, reveals that the gene for flagelliform silk has some marvelous architecture of its own. Like other silk genes, the DNA that codes for flagelliform silk is a repetitive string of nucleotides. But these nucleotides are grouped in a way that may be an engine for generating diversity. Although the finding may not have an immediate impact on the way artificial silk is designed, it has excited people who think about spider evolution. "This structure is totally different from anything we've seen in spiders," says Catherine Craig, an evolutionary biologist at Tufts University in Medford, Massachusetts. "It looks like a system that could allow considerable variation in the composition of flagelliform silk proteins."



Nice threads. *Nephila clavipes* dabs sticky silk onto a framework of elastic flagelliform silk (blue).

Many arthropods make silk: spiders, silkworms, butterflies, and even some honeybees. Trying to mimic and improve this wonder fiber, outfits from the U.S. Army to DuPont have investigated its biomechanics and genetics. Since 1990, several teams have discovered 10 spider silk genes. But no one had looked at the genetics of the highly elastic flagelliform silk, so called because the glands that produce it resemble whips. So evolutionary biologist Cheryl Hayashi and molecular biologist Randolph Lewis of the University of Wyoming, Laramie, sequenced genes for the flagelliform silk of the tropical spiders *Nephila clavipes* and *Nephila madagascariensis*.

Silk proteins are made of repeating amino acid motifs. Some researchers think this chain of springlike helices is a key to the strength and elasticity of silk, and the regularity may help the liquid proteins self-assemble into fibers as they are pulled out of the silk glands. Not surprisingly, as Hayashi and Lewis sequenced the *Flag* gene, they found repeated stretches in the DNA that coded for three regular amino acid motifs. Curiously, these motifs kept turning up in the same order.



But Hayashi and Lewis also came across a stretch that didn't code for amino acids. Such noncoding sequences, or introns, are common in other genes but had never been seen before in spider silk DNA. Then Hayashi found another, and another—almost all the same size. "That's when I started to be surprised," she says. The 12 introns take up about half the gene, and they alternate with active coding regions called exons. Even more unusual, most of the introns are very similar—two of them are 99.9% identical—suggesting that the introns are more highly conserved than the exons, which code for amino acids. That's like taking better care of your CD cases than the compact discs themselves.

Hayashi and Lewis believe that all these peculiarities are tied to the monotony of the exons. When a sequence is highly repetitive, enzymes that copy the DNA can lose their place and make an error. That could explain why the exons tend to vary more in length than do the introns, which are less repetitive. The exons are also rich in the nucleotides cytosine and guanine, which when found in strings may increase the chance of genetic mistakes. Either factor might have led to new genetic diversity, the researchers say.

On the other hand, the repetitive architecture may lead to "homogenization" of the gene, which occurs when one repeat overwrites another repeat. Such rewriting is more likely when the repeats are similar in sequence. "The amazing similarity across the *Flag* introns almost certainly means that this kind of recombination event led to the redundancy of the motifs," says Andrew Clark, an evolutionary geneticist at Pennsylvania State University, University Park.

This tug-of-war between mutation and homogenization may put the spider in a bit of an evolutionary tangle, Hayashi and Lewis say. Although the gene structure may be good for allowing mutations—and coming up with an even better type of silk—the same architecture means that those improvements might be weeded out. "Purely because of the repetitiveness, it might be very hard to stabilize these genes and maintain an optimal sequence," Hayashi says.

Silk is crucial for spiders; aside from catching insects, they also use it as a safety line and to make egg cases. That makes spiders great animals for exploring the link between the evolution of an important behavior and the evolution of a family of proteins, Craig says. And because the protein is directly extruded—rather than hidden inside the body like most proteins—the physical effects of mutations on silk proteins and spider survival are much easier to study. Those kinds of experiments may be far off, but probing the genes behind the proteins is a key step. "Now we know the structure of the gene," Craig says, "and that's fantastic."

–ERIK STOKSTAD

PLANETARY SCIENCE

NEAR Finds a Battered But Unbroken Eros

When the Near Earth Asteroid Rendezvous (NEAR) spacecraft went into orbit around the asteroid Eros last Monday, planetary scientists were expecting to see a body little worn by the ravages of time. According to conventional theory, Eros had escaped from the main belt of asteroids between Mars and Jupiter shortly after it was formed in a catastrophic collision of two larger asteroids. With little time spent in the cosmic shooting gallery of the main belt, Eros should have arrived near Earth less blemished by impacts than siblings that remained behind. But data from NEAR reveal that the asteroid took a heavier beating than expected, NEAR team members announced last week; the pitted surface suggests a slower, unconventional passage out of the main belt. Early NEAR returns also hint at Eros's innermost nature.

Every image returned by the NEAR spacecraft on its arrival shows a surface almost covered with impact craters. The more craters, the longer a body has been exposed to the interplanetary elements, so "Eros does have an ancient surface," says NEAR project scientist Andrew Cheng of the Applied Physics Laboratory (APL) in Laurel, Maryland, which built the space-

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